

Align seq 1/1 to: HG180101 from: 1 to: 974

```

2 GlyLeuSerThrValProAspLeuLeuLeuProLeuValLeuLeuGluLeu 18
|||||
1 GGGTCTTCAGAGGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 50
|||||
18 glcuValGlyLeuTyrProSerGlyValIleGlyLeuValProHisLeuG 35
|||||
51 GTTGTTGGAAATATAAGGTCAGAGGTTATTGGACTGGTGGCTCAGCTAG 100
|||||
35 lysAspArgGluLysAsnAspSerValGlyProGlnGlyLysTyrLeuHis 51
|||||
101 GGACAGGCGAGAGACAGATACGTGGTGGTGGTGGTGGTGGTGGTGGTGG 150
|||||
52 ProGlnAsnSerIleProSerThrLysCysHisLysGlyThrTyrLeu 58
|||||
151 GCTCAAAATAATTCGATTTCGTGTAAGAAATGTCACCAAGAGACCTACTT 200
|||||
68 uTyAsnAspCysProGlyProGlyLeuAspThrAspCysArgGlnCysG 95
|||||
201 GTCAATGATGTCTCAAGAGAGAGAGAGATATATATATATATATATATAT 250
|||||
85 IuSerGlySerPheThrAlaSerGlnAsnHisLeuArgHisCysLeuSer 101
|||||
251 AGACGGCGCTCTTCACCCCTTCACCAAACTACCTCAGACACTGGCTCAG 300
|||||
102 CysSerLysCysArgLysGlnMetGlyGlnValGlnLeuSerSerCysTh 118
|||||
301 TGTCTCAATATGCGAAGAGAAATGGTCAAGTGGAGATGCTCTTCTTCAC 350
|||||
118 rValAspArgAspThrValGlyCysGlyCysArgLysAsnGlnTyrArgHis 135
|||||
351 AGTGAAGGAGATATATGCTGTGAGATATATATATATATATATATATAT 400
|||||
135 yTrpSerGlnAsnLeuPheLeuLysPheAsnLysSerLeuLysLeuAsn 151
|||||
401 ATTCGACAGCAAAACCTTTTCACATTCCTTCATTCATTCGACGCTCGCT 450
|||||
152 GlyThrValHisLeuSerPheSerGlnHisGlnLysGlnAsnThrValGly 168
|||||
451 GGGACGCTGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 500
|||||
168 SHSAlaGlyPheLeuLeuArgGlnAsnGlnCysValSerCysSerAsnG 185
|||||
501 CGATGAGATTTTCTTCAGAAAGAAAGAGAGAGAGAGAGAGAGAGAGAG 550
|||||
185 yLysLysSerLeuGlnCysThrLysLeuCysLeuProGlnIleGlnAsn 201
|||||
551 GTAAGAAAGAGCCGGCAGTGTATGAAAGTTCGTGGCTACCCACAGATTC 600
|||||
202 ValLysGlyThrLysAspArgGlyThrThrValLeuLeuProLeuValG 218
|||||
601 GTTAAGAGAGCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 649
|||||
218 ePheLeuGlyLeuCysLeuSerLeuLeuPheLeuLeuGlyLeuGlyLeu 232
|||||
650 TTCTCTTGATCTTTTGGCTTTTATTCCTCTCTCTCTCTCTCTCTCTCT 693
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seq_name: qb_est1:A0117362

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seq documentation block:
LOCUS      A0117362      889 bp      mRNA      EST      19-OCT-2000
DEFINITION A0117362 HEMBA1 Homo sapiens cDNA clone HEMBA1091229 5', mRNA
sequence.
ACCESSION  A0117462
VERSION    A0117362.1  GI:10942324
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 889)
AUTHORS   Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y.,

```

Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Souda, S. and Isozaki, T.
 HRI human cDNA project
 Unpublished (2000)
 Contact: Takao Isozaki
 Genomics Laboratory
 Helix Research Institute
 1532-4 Yama, Kisarazu, Chiba 292 0812, Japan.
 Tel: 81 438-52-4551
 Fax: 81 438-52-4952
 Email: genomics@hri.co.jp
 HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix
 Research Institute; cDNA library construction; Department of
 Virology, Institute of Medical Science, University of Tokyo, and
 Helix Research Institute.

FEATURES

Source

Location/Qualifiers
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 /organism="Homo sapiens"
 /cell_line="HEMBA1001229"
 /clone_lib="HEMBA1"
 /library_type="Whole embryo, mainly head"
 /map_method="embryo 20 weeks"
 /note="Vector: pMIRSP13"

BASE COUNT 167 a 301 c 249 g 166 t 6 others
 ORIGIN

alignment_scores:

Quality: 1206.00 Length: 229
 Ratio: 5.414 Gaps: 0
 Percent similarity: 99.127 Percent identity: 98.690

alignment_block:

US-09-525-998A.2 x A0117362

Align seq 1/1 to: A0117362 from: 1 to: 889

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223 CysLeuLeuSerLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 239
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4 TGGCTTTTATGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 52
|||||
239 PheSerLysSerLeuGlnValGlySerGlySerThrProGlnGlySer 256
|||||
54 CAGAGTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 102
|||||
256 TGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 122
|||||
104 AGCGGCAAGCTTCAGCGCAAGCTTCAGCGCGCGCGCGCGCGCGCGCGCG 152
|||||
273 PheSerProThrProGlyPheThrProHisLeuGlyPheSerProVal 289
|||||
153 TTGAGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 262
|||||
289 SerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 306
|||||
204 CAGTTCAGCTTCAGCTTCAGCTTCAGCTTCAGCTTCAGCTTCAGCTTCAG 252
|||||
306 suPheAlaAlaProArgArgGlnValAlaAlaProGlyThrThrValAlaAsp 322
|||||
254 ACCTTCGCGCTTCGCGCGCTTCAGAGGCTGGTACACCCCTATCATGGCT 302
|||||
323 ProLysLeuAlaThrAlaLeuAlaSerAspProLysProLysProLeuGln 339
|||||
304 CCGATGCTTCGATGATGATGATGATGATGATGATGATGATGATGATGAT 352
|||||
339 nLysLysLysSerAlaHisLysProGlnSerLeuAspThrAspAspPhe 356
|||||
353 GAACTTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 402
|||||
356 rGAlaThrLeuTyrAlaValValGlnAsnValProLeuAspArgTTCGAG 372
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404 CGCGGCAAGCTTCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 452
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BASE COUNT      134 d
ORIGIN
alignment_scores:
    Quality: 1195.50
    Ratio: 5.198
    Percent Similarity: 96.639
alignment_block:
US-09-525-998A 2 x AC680679

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seq_name: qf_est1:AL522989					
seq_documentation_block:					
LOCUS	AL522989	837 bp	mRNA	EST	13 FEB 2001
DEFINITION	AL522989: TT.NF004.NF02 Homo sapiens KIAA 0136c cDNA sequence.				
	prime, mRNA sequence.				

VERSION AL522984 J 81-13/864HE
KEYWORDS EST.
SOURCE human.
ORGANISM HOMO sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo;
1 (bases 1 to 837)
AUTHORS
Li, W.B., Guher, C., Lessee, J. and Polayes, D.
TITLE
Full-length cDNA libraries and normalization
JOURNAL
Unpublished (2001)
COMMENT
Contact: Genoscope
Genoscope - Centre National de Séquençage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr Web: www.genoscope.cns.fr

FEATURES
Source

1..837
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="csp00004p14"
/clone_lib="L11_NFL004_NBC2"
/sex="male"
/tissue="neuroblastoma cells"
/lab_host="puc19"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with NotI and
cloned into the NotI and EcoRV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed
by life technologies. Contact: Feng Jiang life
technologies, a division of invitrogen 4860 Medical Center
Drive Fosterville, Maryland 20866, USA Fax: (1) 301 610
8371 Email: liliang@life.com URL:
http://fulllength.invitrogen.com"

BASE COUNT 199 a 231 c 229 g 177 t 1 others

alignment_scores
Quality: 1191.00 Length: 213
Ratio: 5.618 Gaps: 0
Percent Similarity: 24.63 Percent Identity: 94.53

alignment_block:

US-09-525-998A-2 x AS522489

Align seq 1/1 to: AS522489 from: 1 to: 837

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198 ATGGAGCTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 47
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17 tleuLeuValGlyTleGlyTleGlyTleGlyTleGlyTleGlyTleGly 34
|||||
248 GCTGCTGGGCAATACCCCTGAGGAGAGAGAGAGAGAGAGAGAGAGAG 297
|||||
34 enGlyAspArgGlyAspArgAspSerValCysProGlnGlyLysTyrIle 50
|||||
298 TAGCGGACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 347
|||||
51 HisProGlnAspAspSerIleCysTyrThrIleCysTyrHisGlyThrTy 67
|||||
348 CAGCTCAAAATATGATGATGATGATGATGATGATGATGATGATGATG 397
|||||
67 tleuTyrAsnAspCysProGlyProGlyGlnAspThrAspCysArgGluC 84
|||||
398 CTGTGTAATCACTGTCACGAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 447
|||||
84 yscIuSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 100
|||||
448 GTACAGGGGCTCTCTACCGCTTCAGAAACCCAGCTACAGACATGCCCT 497
|||||
101 SerCysSerLysCysArgLysCysMetGlyGlnValGlnIleSerSerCy 117
|||||
498 AGCTGCTCAAAATGCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 547
|||||
117 sThrValAspArgAspThrValCysGlyCysArgGlyAsnGlnTyrArgH 134
|||||

548 CACATGGCATCGGACACATCGTGTGTGGTTCATACAAATACAGTACGG 597
|||||
134 tStrIlePheSerGlnAspLeuPheGlnCysPheAspCysSerIleCysLeu 150
|||||
356 ATTATGGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 647
|||||
151 AsnGlyThrValHisLeuSerCysGlnGlnIleCysGlnAsnThrValCys 167
|||||
648 AATGGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 697
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167 rCysHisAlaGlyPhePheLeuArgGlnAsnGlyCysValSerCysSerA 184
|||||
698 GTGGCATGACATTCCTTCTACAGAGAAAGAGAGAGAGAGAGAGAGAG 747
|||||
194 enCysIleCysSerIleCysThrCysLeuCysIleGlnGlnGlnGln 206
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748 ACTGTACAAAGAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAG 797
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201 AsnValGlyThrCysAspSerCysThrThrValThr 213
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798 AATGTAAG 846
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seq_name: qb_est2:ba871809

seq_documentation_block:

seq_id: 969 bp, 969 bp, 969 bp
seq_desc: 1446 x 1.1 kb, 1446 x 1.1 kb, 1446 x 1.1 kb
seq_type: mRNA sequence

ACCESSION BE871809

VERSION BE871809.1

KEYWORDS EST

SOURCE human

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo;

1 (bases 1 to 969)

Author: National Institutes of Health, Mammalian Gene Collection (MGC)

Title: Unpublished (1999)

Journal: National Institutes of Health, Mammalian Gene Collection (MGC)

Comment: Contact: Robert Strausberg, Ph.D.

Email: rstraus@nhi.nih.gov

Tissue: Tissue Procurement: AICC

CNA Library Preparation: Life Technologies, Inc.

CNA Library Arrayed by: The I.M.A.G.E. Consortium (IMI)

DNA Sequencing by: Incyte Genomics, Inc.

Gene Distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/IML at:

http://image.llnl.gov

Plate: HAW574 row: 6 column: 22

High quality sequence step: 642

Location/Qualifiers

1..969

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAG338526"

/clone_lib="NIH MGC 65"

/issue_type="adenocarcinoma"

/lab_host="pH10R (phage-resistant)"

/note="organ: colon; Vector: pCMV-Sport6; Size: 1.1 kb; NotI;

Site: 2; Salt: cloned unidirectionally; Primer: G199 d1;

Average insert size: 1.8 kb; Library constructed by life

technologies."

BASE COUNT 281 a 273 c 241 g 174 t

ORIGIN

alignment_scores

Quality: 1149.50 Length: 284

Ratio: 4.598 Gaps: 0

Percent Similarity: 86.505 Percent Identity: 74.941

alignment_block:

US-09-525-998A-2 x BE871809


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309 aProArqArqGluValAlaProProTyrGlnGlyValAlaAspProIleLeuA 326
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201 TCCCGCGACAGAGGTGGCAGCAGGCTATCCAGCGGGCTCAGCCCATCTTTG 250
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326 GATrAlaLeuAlaSerAspProIleProAsnProLeuGlnIleIleCHe 342
|||||
251 GGCAGGCTCGCTGGCTGGAGTGGATGGATGGATGGATGGATGGATGGATGG 300
|||||
343 AspSerAlaHisIleIleSerIleAspThrAspProAlaThrIle 359
|||||
301 GACAGCGGCCACACGACACAGAGCTATACACTTCATCAGCCCGGACGCT 350
|||||
359 uTyAlaValValGluAsnValProProLeuAlaGlnIleIleIleValAla 376
|||||
351 GACCGCGCTGGCTGGAGAGCGTGGCGCGGCTGGCGTGGAGAAATTCGTGC 400
|||||
376 rTArqGlnIleIleSerAspIleIleIleAspArqGlnIleIleIleIle 392
|||||
401 GCGGCTAGGAGTGGAGGCTGGAGGCTGGAGGCTGGAGGCTGGAGGCTGG 450
|||||
393 GlyArgCysLeuArgGlnAlaGlnIleIleIleIleIleIleIleIleIle 409
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451 GCGGCTCGCTGGCTGGAGAGCGTGGAGAGCGTGGAGAGCGTGGAGAGCG 500
|||||
409 qArqThrProArqArqGluAlaThrLeuGlnLeuLeuGlnValLeuA 426
|||||
501 GCGAGCTGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 550
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426 rTArqPMTAspIleIleIleIleIleIleIleIleIleIleIleIleIle 442
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551 GCGAGTGGAGCTGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 600
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443 GlyProAlaAlaLeuProProAlaPro 451
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501 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 527

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seq_name: qb_est2-BG282718

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seq_documentation_block:
LOCUS      BG282718      761 bp      mRNA      21-SEP-2001
DEFINITION 602406578P1 NIH_MGC_41 Homo sapiens cDNA clone IMAGE 4518690 c.
            mRNA sequence.
ACCESSION  BG282718
VERSION    BG282718.1 GI:13041865
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1. (bases 1 to 761)
            NIH-MGC http://mgi.scripps.edu/
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: rastra@nib.nih.gov
            Tissue Procurement: DCTD/DTF
            CDNA library preparation: Life Technologies, Inc.
            CDNA library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: L1AM10413 row 1 column: 19
            High quality sequence stop: 682.
FEATURES             location/qualifiers
     source           1..761
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4518690"
                     /clone_lib="NIH_MGC_91"
                     /tissue_type="adipocarcinoma, cell line"
                     /lab_host="PH10B (phage-resistant)"
                     /note="organ: prostate, Vector: p.MV SP6K6; Site_1: NotI;

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FEATURES
source

```

Site_2: Salt: Cloned unidirectionally; oligo dT primed;
Average insert size 1.4 kb. Library enriched for
500 length clones and constructed by life technologies.
Note: this is a NIH_MGC library.

BASE COUNT 175 a 228 c 179 g 179 t

ORIGIN

alignment_scores:

Quality: 110.50 Length: 285
Ratio: 4.646 Gaps: 11
Percent Similarity: 83.860 Percent Identity: 78.596

alignment_block:

US-09-525-998A-2 x BG282718

Align: seq 1/2 from: 1 to: 741

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2 AAGTGGCACAAGAGAACTACTTGTACAAAGAGTGTGTGTGTGTGTGTGTGT 51
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77 GAspThrAspCysArgGlnGlySerIleSerIleThrAlaSerGln 93
|||||
52 GGAAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 101
|||||
94 AsnHisSerAlaHisCysIleCysSerCysSerCysSerCysSerCysSer 110
|||||
102 AACGACGTCAGAGACTGGCTCAGACAGTCCGCAAAAGGAAAGGAAAGGAA 151
|||||
110 LysLeuValGlnIleSerSerCysThrValAsnMetAspThrValIleGly 126
|||||
152 GTCAGGTGGAGATCTCTCTCTGGCAGTGGAGAGAGAGAGAGAGAGAGAG 201
|||||
127 CysArgIleCysAsnGlnIleIleIleIleIleIleIleIleIleIleIle 143
|||||
202 TGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 251
|||||
143 sPhrAsnCysSerIleIleIleIleIleIleIleIleIleIleIleIleIle 160
|||||
252 GTTAAATGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 301
|||||
160 LeuLeuGlnAsnIleValCysThrCysHisAlaGlnIlePhePheLeuArg 176
|||||
302 AGAAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 351
|||||
177 AsnIleCysValSerCysSerAsnIleCysSerIleIleIleIleIleIle 193
|||||
252 AAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 376
|||||
193 ystCysSerIleIleIleIleIleIleIleIleIleIleIleIleIleIle 209
|||||
376 ..... 376
210 ThrThrValLeuLeuProLeuValIleIlePheGlyIleIleIleLeuLeu 226
|||||
377 ACCACAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 426
|||||
226 GlnLeuGlnIleIleIleIleIleIleIleIleIleIleIleIleIleIle 242
|||||
427 GGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 476
|||||
243 LeuIleSerIleValCysGlyIleIleIleIleIleIleIleIleIleIle 259
|||||
477 GTTATCTGCAATCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 526
|||||
259 GlnGlyThrThrThrLeuLeuProLeuAlaIleProAspThrSerIle 275
|||||
527 TGAAGGAGACACACACACACACACACACACACACACACACACACACAC 576
|||||
276 ThrProGlyPheThrProIleIleIleIleIleIleIleIleIleIleIle 292
|||||
577 AATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 626

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51  hisProGluAsnSerIleCysThrLysCysHisLysGlyThrTy 67
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370  CACCCCTCAAAATAATTCGATTTCCTGCTACCAAGTCCCAAGAACCACTA 419
67  fLeuTyAsnAspCysProGlyPheGlyGlyAspThrAspCysArgGluC 84
|||||
420  CTTGTACAAATGACTGTCAAGAGGCGGAGGAGGATATGAACTGCAAGAGT 459
84  fSGlucSerClySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 100
|||||
470  GTGAGAGCGGTGTTTATGAGTTTATGAGAAATATCTCAGACATGGCTC 519
101  SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCy 117
|||||
520  AGCTGGTCAAAAGCCCAAGCAAAAGGAGGATACAGCGACAGATCTTCCTG 569
117  sThrValAspAspAspThrValGlyGlyCysArgLysAsnGlnTyArgH 134
|||||
570  CACAGTGAGAGCGAGACACGCTGTGTGGTGTGAGAGAAAGAGTACGCGG 619
134  isTyTrpSerGluAsnLeuPheGlnCysPheAsnCysSerLeuCysLeu 150
|||||
620  ATTATGAGAGCAAAATCTTTTGTAGTGTTCATTTGAGGCTGTGGCTC 669
151  AsnGlyThrValHisLeuSerCysGlnGlnLysGlnAsnThrValCysTh 167
|||||
670  AATCGGACCGTGCACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 719
167  rCysHisAlaGlyPhePheLeuArgGluAsnGluCysValSerCysSerA 184
|||||
720  CTCTATGAGAGGTTTCTTCTTAAAGAGAAATGATGCTGCTGCTGCTGCT 768
184  snCysLysIleSerGluGluCysThrLysLeuCysLeuArgHisCysLeu 200
|||||
769  ACTGTATGAGAAAGCTGATATGAGAGAGTGTGTGTGTGTGTGTGTGTGT 817
201  AsnValLysGlyThrGluAsp 207
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818  ...TGTTAAGGACATGAGGAC 835

seq_name: qb_est1:A0124446
seq_documentation_block:
LOCUS       A0124446      859 bp      mRNA           23-OCT-2000
DEFINITION  A0124446 NT2PM4 Homo sapiens cDNA clone NT2RM4000018 5', mRNA
sequence.
ACCESSION   A0124446
VERSION     A0124446
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS     Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S., Saito,K., Yamamoto,J.,
            Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki,Y., Sugano,S. and
            Isoqai,T.
TITLE       HRI human cDNA project (Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S.,
            Saito,K., Yamamoto,J., Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki
            Y., Sugano,S., Isoqai,T.)
JOURNAL     unpublished (2000)
COMMENT     Contact: Takao Isoqai
            Genomics Laboratory
            Helix Research Institute
            1532-3 Yaba, Kisarazu, Chiba 292-0812, Japan
            Tel: 81-438-52-3951
            Fax: 81-438-52-3952
            Email: genomics-hri.co.jp
            HRI human cDNA project: 5'- & 3'-end one pass sequencing: Helix
            Research Institute, cDNA library construction: Department of
            Virology, Institute of Medical Science, University of Tokyo, and
            Helix Research Institute.

```

FEATURES

source

Location/Qualifiers

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1..859
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="NT2RM4000018"
/cell_line="NT2RM4"
/cell_type="teratocarcinoma"
/cell_line="NT2"
/note="vector: pMT18SFL3; mRNA from uninduced N12 neuronal
precursor cells"
BASE COUNT 197 a 247 c 220 g 192 t 3 others
ORIGIN

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alignment_scores:

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Quality: 1048.00      Length: 194
Ratio: 5.458          Gaps: 0
Percent Similarity: 98.969 Percent Identity: 98.454

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alignment_block:

US-09-525-998A-2 x A0124446

Align seq 1/1 to: A0124446 from: 1 to: 859

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1  MelGlyLeuSerThrValProAspLeuLeuProLeuValLeuLeuGlu 17
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279  ATGGGCTTCCTCCACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 328
17  leuLeuValGlyIleCtyProSerGlyValIleClyLeuValProHisL 34
|||||
329  GTGTGTGAGAGAAATATACTTAAAGGATATGAGATGAGTGGTGGTGG 378
34  euClyAspArgCulysArgAspSerValCysProGlnClyLysTyPhe 50
|||||
379  TAGCGGCACAGGGAGAGACAGATAGTCTGCTGCTGCTGCTGCTGCTGCTG 428
51  HisProGlnAsnAsnSerIleCysCysThrLysCysHisLysGlyThrTy 67
|||||
429  CACCCCTCAAAATAATTCGATTTCCTGCTGCTGCTGCTGCTGCTGCTGCT 478
67  ileuTyAsnAspCysProGlyProGlyClnAspThrAspCysArgGluC 84
|||||
479  CTTGTACAAATGATTTCTGAGGCTGAGGAGAGATATGAGATGAGAGAGT 528
84  ySGlucSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 100
|||||
529  CACAGAGCGGAGTGTCTGCAAGCTTCAGAAACACCTTCAGACACCTGCTC 578
101  SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCy 117
|||||
579  AGCTGCTCCAAATGCCGAGAAAGAAATGGGTCAGGTCAGATCTCTCTTG 628
117  sThrValAspAspAspThrValCysGlyCysArgLysAsnGlnTyArgH 134
|||||
629  CACCTGCAAGAGGATATGAGTGTGAGCTGAGAGAGAGAGAGAGAGAGAG 678
134  isTyTrpSerGluAsnLeuPheGlnCysPheAsnCysSerLeuCysLeu 150
|||||
679  ATTATTCGACCTCAAAAGCTTTCCTGCTGCTGCTGCTGCTGCTGCTGCT 728
151  AsnGlyThrValHisLeuSerCysGlnGlnLysGlnAsnThrValCysTh 167
|||||
729  AATGGGACCGCTGCAAGCTTTCCTGAGAGAAACAGAAACACCTGCTGCT 777
167  rCysHisAlaGlyPhePheLeuArgGluAsnGluCysValSerCysSerA 184
|||||
778  CTAATATGAGAGATTTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 827
184  snCysLysIleSerLeuGluCysThrLysLeu 194
|||||
828  ACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 859

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